

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 27, 2003, 12:55:07 ; Search time 11.0695 Seconds

(without alignments)
2585.358 Million cell updates/sec

Title: US-09-762-767a-2

Sequence: 1 MFCYKLDKIDITGECPSLL.....OKDYEDGNANFICKASGID 690

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Swissprot_40*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3593	100.0	690	1	CYGL_HUMAN
2	3232	90.0	690	1	CYGL_HUMAN
3	3107	86.5	691	1	CYGL_BOVIN
4	1651	46.0	730	1	CYGL_RAT
5	1635	45.5	732	1	CYGL_HUMAN
6	976.5	27.2	683	1	CYGL_DROME
7	795	22.1	619	1	CYGL_RAT
8	793.5	22.1	619	1	CYGL_BOVIN
9	789.5	22.0	619	1	CYGL_HUMAN
10	774.5	21.6	682	1	CYGL_HUMAN
11	708	19.7	617	1	CYGL_HUMAN
12	460	12.8	1047	1	ANPB_BOVIN
13	460	12.8	1047	1	ANPB_HUMAN
14	460	12.8	1047	1	ANPB_RAT
15	457.5	12.7	1057	1	ANPB_RAT
16	456.5	12.7	1061	1	ANPB_HUMAN
17	454.5	12.6	1057	1	ANPB_MOUSE
18	452	12.6	433	1	KSCC_RAT
19	450	12.5	1108	1	CYGL_MOUSE
20	448	12.5	1108	1	CYGL_RAT
21	445	12.4	1109	1	CYGL_CANFA
22	442	12.3	1108	1	CYGL_HUMAN
23	440	12.2	1103	1	CYGL_BOVIN
24	438	12.2	1110	1	CYGL_RAT
25	438	12.2	1110	1	CYGL_BOVIN
26	434	12.1	1103	1	CYGL_HUMAN
27	430	12.0	1110	1	CYGL_RAT
28	428.5	11.9	1050	1	ANPB_HUMAN
29	427	11.9	1125	1	CYGL_MOUSE
30	414.5	11.5	1073	1	HSEK_PTG
31	408.5	11.4	1073	1	HSEK_HUMAN
32	407.5	11.3	1072	1	HSEK_RAT
33	399.5	11.1	1076	1	HSEK_CAVPO

34	389	10.8	1137	1	CYGL_CAEEL	009435 caenorhabditis
35	322.5	9.0	887	1	CYGL_HUMAN	008463 homo sapien
36	322	9.0	1068	1	CYGL_RAT	P26770 ratius norv
37	319.5	8.9	1059	1	CYGL_MOUSE	P26782 mus muscula
38	319	8.9	1090	1	CYGL_RAT	P26763 ratius norv
39	316	8.8	1080	1	CYGL_HUMAN	P26763 homo sapien
40	310.5	8.6	1078	1	CYGL_BOVIN	Q29450 bos taurus
41	303.5	8.4	1144	1	CYGL_HUMAN	O50266 homo sapien
42	303	8.4	1144	1	CYGL_RAT	P21972 ratius norv
43	302	8.4	1134	1	CYGL_BOVIN	P19754 bos taurus
44	290.5	8.1	2248	1	CYGL_DROME	P32870 drosophila
45	287.5	8.0	1249	1	CYGL_MOUSE	P37490 mus muscula

ALIGNMENTS

RESULT 1
ID CYGL_HUMAN STANDARD: PRT: 690 AA.
AC 002108; Q43843;
DT 01-JUL-1993 (rel. 26, Created)
DT 30-MAY-2000 (rel. 39, Last sequence update)
DT 16-OCT-2001 (rel. 40, Last annotation update)
DE Guanylate cyclase soluble, alpha-1 chain (EC 4.6.1.2) (GCS-alpha-1)
DE (Soluble guanylate cyclase large subunit) (GCS-alpha-3).
GN GUCY1A1 OR GUCY1A3 OR GUC1A3 OR GUCSA3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Plimates; Carnivora; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92316204; PubMed=1352257;
RA Guilli G., Scholl U., Bulle F., Guejlaen G.;
RT "Molecular cloning of the cDNAs coding for the two subunits of
RT soluble guanylyl cyclase from human brain.";
RL FEBS Lett. 304:83-86(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Gensmann Y., Bruchhaert P., Fiers M.;
RT "Human soluble guanylate cyclase large subunit mRNA, alpha3-like.";
RL Submitted (Mar-1996) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98416113; PubMed=9742212;
RA Zabel U., Weeger M., La M., Schmidt H.H.;
RT "Human soluble guanylate cyclase: functional expression and revised
RT isoenzyme family.";
RL Biochem. J. 335:51-57(1998).
CC -1- CATALYTIC ACTIVITY: GTP -> 3',5'-cyclic GMP + diphosphate.
CC -1- ENZYME REGULATION: ACTIVATED BY NITRIC OXIDE IN THE PRESENCE OF
CC MAGNESIUM OR MANGANESE IONS.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- MISCELLANEOUS: THERE ARE TWO TYPES OF GUANYLATE CYCLASES: SOLUBLE
CC FORMS AND MEMBRANE-ASSOCIATED RECEPTOR FORMS.
CC -1- SIMILARITY: BELONGS TO GUANYLATE CYCLASE CLASS-4/GUANYLYL CYCLASE
CC FAMILY.
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CC DR EMBL; X66534; CA47145.1; -;
CC EMBL; 058855; AAB94794.1; -;

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OM protein - protein search, using sw model

Run on: June 27, 2003, 12:55:07 ; Search time 9.93048 Seconds
(without alignments)
2583.358 Million cell updates/sec

Title: US-09-762-767a-4

Perfect score: 3231

Sequence: 1 MYGFVNALELVIRNYGPE.....QWFLSRKNTGTEKDDDD 619

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

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SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3231	100.0	619	1	CYGL_HUMAN
2	3206	99.2	619	1	CYGL_BOVIN
3	3188	98.7	619	1	CYGL_RAT
4	987	30.5	682	1	CYGL_RAT
5	927	28.7	617	1	CYGL_HUMAN
6	916	28.4	730	1	CYGL_RAT
7	909.5	28.1	732	1	CYGL_HUMAN
8	793	24.5	690	1	CYGL_RAT
9	789.5	24.4	690	1	CYGL_HUMAN
10	770	23.8	691	1	CYGL_BOVIN
11	712	22.0	683	1	CYGL_BOVIN
12	481.5	14.9	1061	1	ANPA_HUMAN
13	468	14.5	1057	1	ANPA_RAT
14	466	14.4	1057	1	ANPA_MOUSE
15	454.5	14.1	1047	1	ANPA_HUMAN
16	453.5	13.9	1110	1	CYGL_BOVIN
17	450.5	13.6	1110	1	CYGL_MOUSE
18	438.5	13.4	1109	1	CYGL_CANRA
19	433.5	13.4	1109	1	CYGL_MOUSE
20	433	13.3	1108	1	CYGL_RAT
21	428.5	13.2	1050	1	CYGL_HUMAN
22	425	13.1	1108	1	CYGL_HUMAN
23	424	13.1	1103	1	CYGL_HUMAN
24	422.5	13.0	1103	1	CYGL_RAT
25	420	13.0	1103	1	CYGL_BOVIN
26	419	12.9	1110	1	CYGL_RAT
27	415.5	12.7	1137	1	CYGL_RAT
28	410	12.7	433	1	HSER_HUMAN
29	409	12.6	1073	1	HSER_HUMAN
30	405.5	12.5	1073	1	HSER_PIG
31	405	12.5	1072	1	HSER_RAT
32	404	12.5	1072	1	HSER_RAT
33	391	12.1	1125	1	CYGL_STRPT

34	389	12.0	1076	1	HSER_CAVPO
35	345.5	10.7	443	1	CYAL_MYCTU
36	309.5	9.6	1134	1	CYAL_BOVIN
37	308.5	9.5	1248	1	CYAL_RAT
38	302.5	9.4	1251	1	CYAL_HUMAN
39	302.5	9.4	1305	1	CYAL_XENLA
40	301.5	9.3	839	1	CYAL_HUMAN
41	301.5	9.3	1249	1	CYAL_MOUSE
42	300.5	9.3	2248	1	CYAL_DROME
43	289	9.3	858	1	CYAL_DICDI
44	283	9.1	1144	1	CYAL_HUMAN
45	292.5	9.1	1334	1	CYAL_CHICK

ALIGNMENTS

RESULT 1

ID CYGL_HUMAN STANDARD: PRT: 619 AA.

AC 002153: 01-JUL-1993 (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DF 16-OCT-2001 (Rel. 40, Last annotation update)

DE Guanylate cyclase soluble, beta-1 chain (EC 4.6.1.2) (CCS-beta-1)

DE (soluble guanylate cyclase small subunit) (CCS-beta-3).

GN GUCY1B1 OR GUCY1B3 OR GUC1B3 OR GUC1B3

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

OX NCBI_Taxid-9606;

RN [1] SEQUENCE FROM N.A. (ISOFORM HSCC-2).

RP TISSUE-KIDNEY; Gansseman Y., Brouckaert P., Fiers W.;

RL Submitted (MGC-1997) to the EMBL/GenBank/DBJ databases.

RC TISSUE-LUNG; MEDLINE-9208652; PubMed-1680753;

RA Chhajlani V., Friendberg P.-A., Ahlner J., Axelsson K.L.,

RT Heterogeneity in human soluble guanylate cyclase due to alternative

RT splicing. FEBS Lett. 290:157-158(1991).

RL FEBS Lett. 290:157-158(1991).

CC -1- CATALYTIC ACTIVITY: GTP -> 3',5'-cyclic GMP + diphosphate.

CC -1- ENZYME REGULATION: ACTIVATED BY NITRIC OXIDE IN THE PRESENCE OF

CC MAGNESIUM OR MANGANESE IONS.

CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.

CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; HSCC-1 (SHOWN HERE) AND HSCC-2;

CC ARE PRODUCED BY ALTERNATIVE SPLICING.

CC -1- MISCELLANEOUS: THERE ARE TWO TYPES OF GUANYLATE CYCLASES: SOLUBLE

CC FORMS AND MEMBRANE-ASSOCIATED RECEPTOR FORMS.

CC -1- SIMILARITY: BELONGS TO GUANYLATE CYCLASE CLASS-4/GUANYLATE CYCLASE

CC FAMILY.

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CC or send an email to license@isb-sib.ch).

DR EMBL: X65533; CAA7144.1; -
 DR EMBL: AF020340; MAB94877.1; -
 DR PIR: S23097; S23097.
 DR HSSP: P15068; 1AMN.
 DR Genew: HGNC:4687; GUCY1B3.
 DR MIM: 139397; -
 DR InterPro: IPR001054; G_cyclase.
 DR Pfam: PF00211; guanylate_cyc; 1.
 DR SMART: SM00044; CYC; 1.
 DR PROSITE: PS00452; GUANYLATE_CYCLASES_1; 1.
 DR PROSITE: PS0125; GUANYLATE_CYCLASES_2; 1.
 DR Lyase: cGMP synthetase; Alternative splicing.
 FT DOMAIN 421 425 GUANYLATE CYCLASE.
 FT VARSPLIT 393 425 MISSING (IN ISOFORM HSCG-2).
 SQ SEQUENCE 619 AA: 70514 MW: 231E4E60DE02AA1 CRC64;

Query Match 100.0%; Score 3231; DB 1; Length 619;
 Best Local Similarity 100.0%; Pred. No. 2e-215;
 Matches 619; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYGFVNALELLVIRNNGPEWEDIKKEAQLDEEGQFLVRIIYDSKTYDLVAASKVLN 60
 DB 1 MYGFVNALELLVIRNNGPEWEDIKKEAQLDEEGQFLVRIIYDSKTYDLVAASKVLN 60
 QY 61 LNAEILQMFGRKPFVFCOESGYDTILRVLSNVREFLQNDALHDLATYPMKRAPSE 120
 DB 61 LNAEILQMFGRKPFVFCOESGYDTILRVLSNVREFLQNDALHDLATYPMKRAPSE 120
 QY 121 RCTDAKRGKGLIHYSEREGLODIYGIKTYAQOIHGTETIDMKVYIQARNEBDHFOFL 180
 DB 121 RCTDAKRGKGLIHYSEREGLODIYGIKTYAQOIHGTETIDMKVYIQARNEBDHFOFL 180
 QY 121 RCTDAKRGKGLIHYSEREGLODIYGIKTYAQOIHGTETIDMKVYIQARNEBDHFOFL 180
 DB 121 RCTDAKRGKGLIHYSEREGLODIYGIKTYAQOIHGTETIDMKVYIQARNEBDHFOFL 180
 QY 181 IEKESKEDFYEDLDREENGQESRISPTFCAPPHIIFEDRLVYTCGNATRYL 240
 DB 181 IEKESKEDFYEDLDREENGQESRISPTFCAPPHIIFEDRLVYTCGNATRYL 240
 QY 181 IEKESKEDFYEDLDREENGQESRISPTFCAPPHIIFEDRLVYTCGNATRYL 240
 DB 181 IEKESKEDFYEDLDREENGQESRISPTFCAPPHIIFEDRLVYTCGNATRYL 240
 QY 241 POLQPGNCSLSVFSLVPRHIDISPHGISINITYVLRSEGLDVEKLECEDELVTGE 300
 DB 241 POLQPGNCSLSVFSLVPRHIDISPHGISINITYVLRSEGLDVEKLECEDELVTGE 300
 QY 241 POLQPGNCSLSVFSLVPRHIDISPHGISINITYVLRSEGLDVEKLECEDELVTGE 300
 DB 241 POLQPGNCSLSVFSLVPRHIDISPHGISINITYVLRSEGLDVEKLECEDELVTGE 300
 QY 301 ISCLRLKGMITYPEADSLIFLCSPSVANLDDLTRRGYLSIDYPLMDATRDVLQEGPR 360
 DB 301 ISCLRLKGMITYPEADSLIFLCSPSVANLDDLTRRGYLSIDYPLMDATRDVLQEGPR 360
 QY 301 ISCLRLKGMITYPEADSLIFLCSPSVANLDDLTRRGYLSIDYPLMDATRDVLQEGPR 360
 DB 301 ISCLRLKGMITYPEADSLIFLCSPSVANLDDLTRRGYLSIDYPLMDATRDVLQEGPR 360
 QY 361 EEKTKQELTLDRLQTLRALDEKERTDTLYSVLPSPVANLDEKRPVAKRYDNY 420
 DB 361 EEKTKQELTLDRLQTLRALDEKERTDTLYSVLPSPVANLDEKRPVAKRYDNY 420
 QY 361 EEKTKQELTLDRLQTLRALDEKERTDTLYSVLPSPVANLDEKRPVAKRYDNY 420
 DB 361 EEKTKQELTLDRLQTLRALDEKERTDTLYSVLPSPVANLDEKRPVAKRYDNY 420
 QY 421 TILPSGIVGFNAFCSHASGEBAKTYVNLNDLTTRDTLDSKNPFYKVTGDKYM 480
 DB 421 TILPSGIVGFNAFCSHASGEBAKTYVNLNDLTTRDTLDSKNPFYKVTGDKYM 480
 QY 421 TILPSGIVGFNAFCSHASGEBAKTYVNLNDLTTRDTLDSKNPFYKVTGDKYM 480
 DB 421 TILPSGIVGFNAFCSHASGEBAKTYVNLNDLTTRDTLDSKNPFYKVTGDKYM 480
 QY 481 TVSGLPSPCIHARSICHLADMEIAGOVQDESVOITGIGTGVYGVIGQMPRY 540
 DB 481 TVSGLPSPCIHARSICHLADMEIAGOVQDESVOITGIGTGVYGVIGQMPRY 540
 QY 481 TVSGLPSPCIHARSICHLADMEIAGOVQDESVOITGIGTGVYGVIGQMPRY 540
 DB 481 TVSGLPSPCIHARSICHLADMEIAGOVQDESVOITGIGTGVYGVIGQMPRY 540
 QY 541 CLEGNVNTLSRTETGEGRTVSEGYRCLAMPENDPOPHLEHGPVSMGKREPMQ 600
 DB 541 CLEGNVNTLSRTETGEGRTVSEGYRCLAMPENDPOPHLEHGPVSMGKREPMQ 600
 QY 541 CLEGNVNTLSRTETGEGRTVSEGYRCLAMPENDPOPHLEHGPVSMGKREPMQ 600
 DB 541 CLEGNVNTLSRTETGEGRTVSEGYRCLAMPENDPOPHLEHGPVSMGKREPMQ 600
 QY 601 VMLSRKNTGETEKODD 619
 DB 601 VMLSRKNTGETEKODD 619

RESULT 2

ID CYG1_BOVIN STANDARD; PRT; 619 AA.
 AC P16068;
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 18-OCT-2001 (Rel. 40, Last annotation update)
 DE Guanylate cyclase soluble, beta-1 chain (EC 4.6.1.2) (GCS-beta-1)

DE (Soluble guanylate cyclase small subunit).
 GN GUCY1B1 OR GUCY1B3 OR GUCY1B3.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN (1)
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Lung;
 RX MEDLINE=8903114; PubMed=2903071;
 RA Koesling D., Herz J., Gausepohl H., Nitroand F., Hirsch K.-D.,
 RA Muelach A., Boehme E., Schultz G., Frank R.;
 RT "The primary structure of the 70 kDa subunit of bovine soluble
 RT guanylate cyclase".
 RL FEBS Lett. 239:29-34(1988).
 RN (2)
 RP 3D-STRUCTURE MODELING OF 412-572.
 RX MEDLINE=98054247; PubMed=9391039;
 RA Liu Y., Ruohe A.E., Rao V.D., Hurley J.H.;
 RT "Catalytic mechanism of the adenylyl and guanylyl cyclases: modeling
 RT and mutational analysis".
 RL Proc. Natl. Acad. Sci. U.S.A. 94:13414-13419(1997).
 CC -1- CATALYTIC ACTIVITY: GTP -> 3',5'-cyclic GMP + diphosphate.
 CC -1- ENZYME REGULATION: ACTIVATED BY NITRIC OXIDE IN THE PRESENCE OF
 CC MAGNESIUM OR MANGANESE IONS.
 CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: LONG AND BRAIN.
 CC -1- MISCELLANEOUS: THERE ARE TWO TYPES OF GUANYLATE CYCLASES: SOLUBLE
 CC -1- FORMS AND MEMBRANE-ASSOCIATED RECEPTOR FORMS.
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 CC -----
 DR EMBL: Y00770; CAA68739.1; -
 DR PIR: S01653; OYB070.
 DR PDB: 1AMN; 28-JAN-98.
 DR InterPro: IPR001054; G_cyclase.
 DR Pfam: PF00211; guanylate_cyc; 1.
 DR SMART: SM00044; CYC; 1.
 DR PROSITE: PS00452; GUANYLATE_CYCLASES_1; 1.
 DR PROSITE: PS0125; GUANYLATE_CYCLASES_2; 1.
 DR Lyase: cGMP synthetase; 3D-structure.
 FT DOMAIN 421 554 GUANYLATE CYCLASE.
 SQ SEQUENCE 619 AA: 70502 MW: 8E9149528B0F344 CRC64;

Query Match 99.28; Score 3206; DB 1; Length 619;
 Best Local Similarity 99.08%; Pred. No. 1e-213;
 Matches 613; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 MYGFVNALELLVIRNNGPEWEDIKKEAQLDEEGQFLVRIIYDSKTYDLVAASKVLN 60
 DB 1 MYGFVNALELLVIRNNGPEWEDIKKEAQLDEEGQFLVRIIYDSKTYDLVAASKVLN 60
 QY 61 LNAEILQMFGRKPFVFCOESGYDTILRVLSNVREFLQNDALHDLATYPMKRAPSE 120
 DB 61 LNAEILQMFGRKPFVFCOESGYDTILRVLSNVREFLQNDALHDLATYPMKRAPSE 120
 QY 121 RCTDAKRGKGLIHYSEREGLODIYGIKTYAQOIHGTETIDMKVYIQARNEBDHFOFL 180
 DB 121 RCTDAKRGKGLIHYSEREGLODIYGIKTYAQOIHGTETIDMKVYIQARNEBDHFOFL 180
 QY 121 RCTDAKRGKGLIHYSEREGLODIYGIKTYAQOIHGTETIDMKVYIQARNEBDHFOFL 180
 DB 121 RCTDAKRGKGLIHYSEREGLODIYGIKTYAQOIHGTETIDMKVYIQARNEBDHFOFL 180
 QY 181 IEKESKEDFYEDLDREENGQESRISPTFCAPPHIIFEDRLVYTCGNATRYL 240
 DB 181 IEKESKEDFYEDLDREENGQESRISPTFCAPPHIIFEDRLVYTCGNATRYL 240
 QY 181 IEKESKEDFYEDLDREENGQESRISPTFCAPPHIIFEDRLVYTCGNATRYL 240
 DB 181 IEKESKEDFYEDLDREENGQESRISPTFCAPPHIIFEDRLVYTCGNATRYL 240